

SID 7

RESULT 2
AX026712
LOCUS AX026712 50 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 14 from Patent WO0039300.
ACCESSION AX026712
VERSION AX026712.1 GI:10187879
KEYWORDS .
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequence.
REFERENCE 1 (bases 1 to 50)
AUTHORS Archer, J.A. and Tuerck, J.A.
TITLE Control of gene expression in eukaryotes
JOURNAL Patent: WO 0039300-A 14 06-JUL-2000;
CAMBRIDGE ADVANCED TECH (GB)
FEATURES Location/Qualifiers
source 1. .50
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="CaMVop2"
BASE COUNT 14 a 18 c 9 g 9 t
ORIGIN

Query Match 100.0%; Score 28; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.073;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tccactgacgtaagggatgacgcacaat 28
|||||
Db 1 TCCACTGACGTAAGGGATGACGCACAAT 28

RESULT 3
AR130348
LOCUS AR130348 98 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 3 from patent US 6187996.
ACCESSION AR130348
VERSION AR130348.1 GI:14118245
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 98)
AUTHORS Ishige, F., Chua, N. and Oeda, K.
TITLE Plant promoter comprising a G-box element, GCCACGTGCC or
GCCACGTGAG, and an application thereof
JOURNAL Patent: US 6187996-A 3 13-FEB-2001;
FEATURES Location/Qualifiers
source 1. .98
/organism="unknown"
BASE COUNT 27 a 27 c 19 g 25 t
ORIGIN

Query Match 100.0%; Score 28; DB 6; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.067;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tccactgacgtaagggatgacgcacaat 28
|||||
Db 4 TCCACTGACGTAAGGGATGACGCACAAT 31

RESULT 4

E13108

LOCUS E13108 98 bp DNA linear PAT 24-JUN-1998

DEFINITION 35S promoter.

ACCESSION E13108

VERSION E13108.1 GI:3251920

KEYWORDS JP 1997131187-A/3.

SOURCE unidentified.

ORGANISM unidentified

unclassified.

REFERENCE 1 (bases 1 to 98)

AUTHORS Ishige,I., Chiyua,N. and Oita,K. .

TITLE PLANT PROMOTER AND ITS UTILIZATION

JOURNAL Patent: JP 1997131187-A 3 20-MAY-1997;

SUMITOMO CHEM CO LTD

COMMENT OS Unknown

PN JP 1997131187-A/3

PD 20-MAY-1997

PF 07-JUN-1996 JP 1996145492

PR 14-JUL-1995 JP 95P 178730, 05-SEP-1995 JP 95P 227967 PI

ISHIGE IKUJI, CHIYUA NAMUOHAI, OITA KENJI

PC C12N15/09,A01H5/00,C07H21/04,C12N5/10,(C12N5/10,C12R1:91); CC
strandedness: Double;

CC topology: Linear;

FH Key Location/Qualifiers

FH

FT source 1. .98

FT /organism='Unclassified'.

FEATURES Location/Qualifiers

source 1. .98

/organism="unidentified"

/db_xref="taxon:32644"

BASE COUNT 27 a 27 c 19 g 25 t

ORIGIN

Query Match 100.0%; Score 28; DB 6; Length 98;

Best Local Similarity 100.0%; Pred. No. 0.067;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tccactgacgtaagggatgacgcacaat 28
|||||
Db 4 TCCACTGACGTAAGGGATGACGCACAAT 31

RESULT 5

AR130349

LOCUS AR130349 102 bp DNA linear PAT 16-MAY-2001

DEFINITION Sequence 4 from patent US 6187996.

ACCESSION AR130349

VERSION AR130349.1 GI:14118246
 KEYWORDS .
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.
 REFERENCE 1 (bases 1 to 102)
 AUTHORS Ishige,F., Chua,N. and Oeda,K.
 TITLE Plant promoter comprising a G-box element, GCCACGTGCC or
 GCCACGTGAG, and an application thereof
 JOURNAL Patent: US 6187996-A 4 13-FEB-2001;
 FEATURES Location/Qualifiers
 source 1. .102
 /organism="unknown"
 BASE COUNT 28 a 27 c 21 g 26 t
 ORIGIN

Query Match 100.0%; Score 28; DB 6; Length 102;
 Best Local Similarity 100.0%; Pred. No. 0.067;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tccactgacgtaagggatgacgcacaat 28
 ||||||||||||||||||
 Db 8 TCCACTGACGTAAGGGATGACGCACAAT 35

RESULT 6
 AR130350/c
 LOCUS AR130350 102 bp DNA linear PAT 16-MAY-2001
 DEFINITION Sequence 5 from patent US 6187996.
 ACCESSION AR130350
 VERSION AR130350.1 GI:14118247
 KEYWORDS .
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.
 REFERENCE 1 (bases 1 to 102)
 AUTHORS Ishige,F., Chua,N. and Oeda,K.
 TITLE Plant promoter comprising a G-box element, GCCACGTGCC or
 GCCACGTGAG, and an application thereof
 JOURNAL Patent: US 6187996-A 5 13-FEB-2001;
 FEATURES Location/Qualifiers
 source 1. .102
 /organism="unknown"
 BASE COUNT 26 a 20 c 28 g 28 t
 ORIGIN

Query Match 100.0%; Score 28; DB 6; Length 102;
 Best Local Similarity 100.0%; Pred. No. 0.067;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tccactgacgtaagggatgacgcacaat 28
 ||||||||||||||||||
 Db 99 TCCACTGACGTAAGGGATGACGCACAAT 72



RESULT 4

AAQ12193

ID AAQ12193 standard; DNA; 40 BP.

XX

AC AAQ12193;

XX

DT 11-SEP-1991 (first entry)

XX

DE ASF-1 binding site from CaMV 35S wild-type promoter.

XX

KW Activation sequence factor 1; ASF-1; roots; ss.

XX

OS Cauliflower mosaic virus.

XX

FH Key Location/Qualifiers

FT misc_binding 5..32

FT /*tag= a

FT /label= protected region detected by DNase I

FT footprinting

FT protein_bind 8..28

FT /*tag= b

FT /label= ASF-1 binding site

FT CAAT_signal 6..9

FT /*tag= c

FT CAAT_signal 28.31

FT /*tag= d

FT repeat_unit 9..13

FT /*tag= e

FT repeat_unit 21..25

FT /*tag= f

XX

PN US5023179-A.

XX

PD 11-JUN-1991.

XX

PF 14-NOV-1988; 88US-0272169.

XX

PR 14-NOV-1988; 88US-0272169.

XX

PA (LAME/) LAM E.

XX

PI Lam E, Benfey PN, Gilmartin PM, Chua NH;

XX

DR WPI; 1991-192554/26.

XX

PT Nucleotide promoter sequence improving gene expression in roots -

PT is binding site for activation sequence factor, isolated from

PT CaMV 35S promoter.

XX

PS Claim 1; Fig 2; 8pp; English.

XX

CC The sequence represents nucleotides -90 -> -50 of the CaMV 35S
CC promoter. The binding site for the AFS-1, a protein isolated from
CC aetiolated peas, has been localised to a 21 bp sequence which
CC includes the two pentanucleotide repeats. Studies of deletion and
CC substitution mutants revealed that binding is abolished by mutation
CC of these repeats but is unchanged or enhanced by mutation of the two

CC CAAT boxes. The promoter sequence enhances expression of genes in
CC roots and can used to alter the specificity of other plant promoters.
CC Insertion of the sequence at posn. -55 of the RUBISCO 3A promoter
CC (specific for green tissue) or introduction by mutation in this
CC region causes substantial expression in roots.
CC See also AAQ12194 and AAQ12195.
XX
SQ Sequence 40 BP; 12 A; 13 C; 7 G; 8 T; 0 other;

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	28	100.0	28	6	AX207054	AX207054 Sequence
	2	28	100.0	50	6	AX026712	AX026712 Sequence
	3	28	100.0	98	6	AR130348	AR130348 Sequence
	4	28	100.0	98	6	E13108	E13108 35S promote
	5	28	100.0	102	6	AR130349	AR130349 Sequence
c	6	28	100.0	102	6	AR130350	AR130350 Sequence
	7	28	100.0	102	6	E13109	E13109 Plant promo
c	8	28	100.0	102	6	E13110	E13110 Plant promo
	9	28	100.0	113	6	AR084230	AR084230 Sequence
	10	28	100.0	113	6	I90373	I90373 Sequence 17
c	11	28	100.0	117	6	AR084231	AR084231 Sequence
c	12	28	100.0	117	6	I90374	I90374 Sequence 18
	13	28	100.0	174	8	AF434749	AF434749 Zea mays
	14	28	100.0	189	6	AX164073	AX164073 Sequence
c	15	28	100.0	197	8	AF434747	AF434747 Zea mays
c	16	28	100.0	198	6	AX207117	AX207117 Sequence
	17	28	100.0	199	8	AF434746	AF434746 Zea mays
	18	28	100.0	199	8	AF434748	AF434748 Zea mays
c	19	28	100.0	199	8	AF434750	AF434750 Zea mays
	20	28	100.0	206	6	AX247517	AX247517 Sequence
	21	28	100.0	210	14	S51061	S51061 35S {promot
	22	28	100.0	240	6	AX033493	AX033493 Sequence
	23	28	100.0	309	6	AX044092	AX044092 Sequence
	24	28	100.0	314	6	AX207114	AX207114 Sequence
	25	28	100.0	331	6	BD001990	BD001990 A transge
	26	28	100.0	332	6	E01311	E01311 Cauliflower
	27	28	100.0	333	6	I04847	I04847 Sequence 3
	28	28	100.0	348	6	AX207116	AX207116 Sequence
	29	28	100.0	354	12	ARCAMVPR	X04879 CaMV promot
c	30	28	100.0	390	12	SCO308514	AJ308514 Synthetic
c	31	28	100.0	392	6	AX207113	AX207113 Sequence
	32	28	100.0	413	6	AX207112	AX207112 Sequence
c	33	28	100.0	423	14	CMV7626	AJ007626 Culiflowe
	34	28	100.0	439	6	A41016	A41016 Sequence 3
	35	28	100.0	439	6	AR082579	AR082579 Sequence
	36	28	100.0	439	6	I28254	I28254 Sequence 3
	37	28	100.0	446	6	A78762	A78762 Sequence 23
	38	28	100.0	446	6	AR014735	AR014735 Sequence
	39	28	100.0	470	6	AX026717	AX026717 Sequence
	40	28	100.0	480	12	SYNCAMVCM5	M74305 Synthetic e
c	41	28	100.0	485	14	CMV7625	AJ007625 Cauliflow
	42	28	100.0	532	6	AR110594	AR110594 Sequence
	43	28	100.0	532	6	AR150993	AR150993 Sequence
	44	28	100.0	532	6	AR152416	AR152416 Sequence
	45	28	100.0	532	6	AR152425	AR152425 Sequence